Claims

1. A method for determining an abundance of a biomolecule in a biological sample, said method comprising the steps of:

(a) adhering a first biological sample to a first support to create a first matrix comprising one or more biomolecules from said first sample;

(b) adhering a second biological sample to a second support to create a second matrix comprising one or more biomolecules from said second sample;

(c) exposing a library of binding species at least one time to said first matrix to create a first product comprising one or more binding species of said library; and

(d) exposing the first product at least one time to said second matrix to create a second product, wherein a binding species present or absent in said second product is indicative of the abundance of said biomolecule in said first biological sample relative to said second biological sample.

2. The method of claim 1, further comprising the steps of:

(e) exposing said library to said second matrix to create a third product comprising one or more binding species of said library; and

(f) exposing the third product at least one time to said first matrix to create a fourth product, wherein a binding species present or absent in said fourth product is indicative of the abundance of said biomolecule in said second biological sample relative to said first biological sample.

3. The method of claim 2, further comprising the step of

(g) comparing said second and fourth products to determine the abundance of said biomolecule in said first sample relative to said second sample.

4. The method of claim 2, further comprising the steps of:

(g) combining the second and fourth products to produce a pooled product;

(h) adhering at least a portion of the pooled product to a third support to provide a third matrix;

(i) exposing said first biological sample at least one time to said third matrix to provide a fifth product;

(j) exposing said second biological sample at least one time to said third matrix to provide a sixth product; and

(k) comparing said fifth and sixth products to determine the abundance of said biomolecule in said first sample relative to said second sample.

5. The method of claim 1, 2, 3, or 4, wherein said first product consists essentially of one or more binding species that bind to said first matrix, or said first product consists essentially of one ore more binding species that do not bind to said first matrix.

6. The method of claim 5, further comprising controlling the relative amount of binding species exposed to said one or more biomolecules of said first matrix in step (c).

7. The method of claim 6, wherein said controlling occurs by preparing a dilution of said first biological sample and creating said first matrix from said dilution.

8. The method of claim 7, wherein steps (a) – (k) are repeated, wherein in each iteration, a different dilution is employed to create said first matrix.

9. The method of claim 6, wherein said controlling occurs by preparing a dilution of said library and exposing said dilution to said first matrix.

10. The method of claim 9, wherein steps (c) – (k) are repeated, wherein in each iteration, a different dilution is exposed to said first matrix.

11. The method of claim 1, 2, 3, or 4, wherein said second product consists essentially of one or more binding species that bind to said second matrix, or said second product consists essentially of one or more binding species that do not bind to said second matrix.

12. The method of claim 11, further comprising controlling the relative amount of binding species exposed to said one or more biomolecules of said second matrix in step (e).

13. The method of claim 12, wherein said controlling occurs by preparing a dilution of said second biological sample and creating said second matrix from said dilution.

14. The method of claim 13, wherein steps (a) – (k) are repeated, wherein in each iteration, a different dilution is employed to create said second matrix.

15. The method of claim 12, wherein said controlling occurs by preparing a dilution of said library and exposing said dilution to said second matrix.

16. The method of claim 15, wherein steps (c) – (k) are repeated, wherein in each iteration, a different dilution is exposed to said second matrix.

17. The method of claim 2, 3, or 4, wherein said third product consists essentially of one or more binding species that bind to said second matrix, or said third product consists essentially of one or more binding species that do not bind to said second matrix.

18. The method of claim 2, 3, or 4, wherein said fourth product consists essentially of one or more binding species that bind to said first matrix, or said fourth product consists essentially of one or more binding species that do not bind to said first matrix.

19. The method of claim 4, wherein said fifth product consists essentially of one or more biomolecules that bind to said third matrix, and said fifth product consists essentially of one or more biomolecules that do not bind to said third matrix.

20. The method of claim 4, wherein said sixth product consists essentially of one or more biomolecules that bind to said third matrix, or said sixth product consists essentially of one or more biomolecules that do not bind to said third matrix.

21. The method of claim 1, 2, 3, or 4, wherein said biomolecule is a protein, nucleic acid, carbohydrate, fatty acid, lipid, steroid, prostaglandin, prostacyclin, or small organic molecule.

22. The method of claim 1, 2, 3, or 4, wherein, prior to step (a), one or more biomolecules in said first biological sample is derivatized with a derivatizing agent in order to enable adhesion to said first support.

23. The method of claim 22, wherein the extent of derivatization is controlled by the type of derivatizing agent, the concentration of the derivatizing agent or the one or more biomolecules, the temperature, or time of reaction.

24. The method of claim 1, 2, 3, or 4, wherein, prior to step (b), one or more biomolecules in said second biological sample is derivatized in order to enable adhesion to said second support.

25. The method of claim 24, wherein the extent of derivatization is controlled by the type of derivatizing agent, the concentration of the derivatizing agent or the one or more biomolecules, the temperature, or time of reaction.

26. The method of claim 1, 2, 3, or 4, wherein said library is a peptide-nucleic acid coupled library, a nucleic acid library, a carbohydrate library, or a small organic molecule library.

27. The method of claim 1, 2, 3, or 4, wherein said peptide-nucleic acid library is a phage display library.

28. The method of claim 1, 2, 3, or 4, wherein said phage display library is an antibody library, a recombinant display library, or a synthetic peptide library.

29. The method of claim 1, 2, 3, or 4, wherein said first biological sample is from a first organism, and said second biological sample is from a second organism.

30. The method of claim 1, 2, 3, or 4, wherein said first and second organisms are humans.

31. The method of claim 1, 2, 3, or 4, wherein said first organism is diseased, and said second organism is healthy.

32. The method of claim 1, 2, 3, or 4, wherein said first organism has been exposed to a chemical agent, and said second organism has not been exposed to said chemical agent.

33. The method of claim 1, 2, 3, or 4, wherein said biological sample is selected from the group consisting of a tissue, a bodily fluid, a cultured cell, and an organ.

34. The method of claim 1, 2, 3, or 4, wherein said tissue or said cultured cell is selected from the group consisting of epithelial, connective, muscle, and nerve tissues or cells.

35. The method of claim 1, 2, 3, or 4, wherein said body fluid is selected from the group consisting of cerebrospinal fluid (CSF), blood, saliva, mucous, tears, pancreatic juice, seminal fluid, sweat, milk, bile, plasma, serum, lymph, urine, pleural effusions, bronchial lavage, ascites, and synovial fluid.

36. The method of claim 1, 2, 3, or 4, wherein said bodily fluid is CSF.

37. The method of claim 1, 2, 3, or 4, wherein said organ is selected from the group consisting of skin, bone, cartilage, tendon, ligament, skeletal muscle, smooth muscle, heart, blood, blood vessel, brain, spinal cord, peripheral nerve, nose, trachea, lung, mouth, esophagus, stomach, intestine, kidney, uterus, ureters, urethra, bladder, hypothalamus, pituitary, thyroid, pancreas, adrenal gland, ovary, oviduct, vagina, mammary gland, testicle, seminal vesicle, penis, lymph, lymph node, lymph vessel, white blood cell, T-cell and B-cell.

38. The method of claim 1, 2, 3, or 4, wherein said first matrix comprises one or more biomolecules from said first biological sample covalently bound to said first support.

39. The method of claim 1, 2, 3, or 4, wherein said second matrix comprises one or more biomolecules from said second biological sample covalently bound to said second support.

40. The method of claim 4, wherein said third matrix comprises one or more binding species from said library covalently bound to said third support.

41. The method of claim 1, 2, 3, or 4, wherein prior to step (a), said first biological sample is treated to denature said biomolecule.

42. The method of claim 1, 2, 3, or 4, wherein prior to step (b), said second biological sample is treated to denature said biomolecule.

43. The method of claim 1, 2, 3, or 4, wherein said exposing in step (c) or step (d) occurs more than once.

44. The method of claim 2, 3, or 4, wherein said exposing in step (e) or step (f) occurs more than once.

45. The method of claim 4, wherein said exposing in step (i) or step (j) occurs more than once.

46. The method of claim 1, 2, 3, or 4, wherein said first, second, or third support comprises a column.

47. The method of claim 1, 2, 3, or 4, wherein said first, second, or third support comprises a chip.

48. The method of claim 3 or 4, wherein said comparing comprises mass spectrometry.

49. The method of claim 3 or 4, wherein said comparing comprises nuclear magnetic resonance spectroscopy.

50. The method of claim 4, wherein prior to step (h) said pooled product is amplified.

51. The method of claim 1, 2, 3, or 4, wherein a difference in the relative abundance of said biomolecule between said first and second biological samples is indicative of a candidate therapeutic target.

52. The method of claim 1, 2, 3, or 4, wherein a difference in the relative abundance of said biomolecule between said first and second biological samples is indicative of a disease state.